X_2 is a hydrophobic residue;

X_3 is an acidic or an aliphatic residue;

X_4 is a basic residue;

X_5 is an apolar residue;

X_6 is an aromatic residue;

X_7 is a polar residue;

X_8 is an aliphatic residue;

X_9 is an acidic or an aliphatic residue;

X_{10} is an aromatic residue;

X_{11} is an aromatic residue;

X_{12} is a polar residue;

X_{13} is Ile;

X_{14} is an apolar residue;

X_{15} is an acidic residue;

X_{16} is a polar residue;

X_{17} is a basic or an aliphatic residue;

Z_1 is H_2N-, RHN- or, RRN-;

Z_2 is -C(O)R, -C(O)OR, -C(O)NHR, -C(O)NRR;

each R is independently (C_1-C_6) alkyl, (C_1-C_6) alkenyl, (C_1-C_6) alkynyl, substituted (C_1-C_6) alkyl, substituted (C_1-C_6) alkenyl or substituted (C_1-C_6) alkynyl;

each "—" between residues Z_1 and X_1 and residues Z_2 and X_{17} represents a covalent linkage; and

each "—" between residues X_1 through X_{17} represents a covalent linkage,

wherein the compound reduces cell-associated binding of transferrin as measured in an *in vitro* cellular binding assay and produces at least an additive effect with soluble HFE/β_2m heterodimers in reducing cell-associated binding of transferrin as measured in the assay.

15. (New) The method of Claim 14, wherein:

X_1 is an apolar amino acid;

X_2 is an aromatic amino acid;

X_3 is an acidic amino acid;

X_4 is a basic amino acid;

X_5 is an apolar amino acid;

X_6 is an aromatic amino acid;

X_7 is a polar amino acid;

X_8 is a aliphatic amino acid;

X_9 is a an acidic amino acid;

X_{10} is an aromatic amino acid;

X_{11} is an aromatic amino acid;

X_{12} is a polar amino acid;

X_{13} is Ile;

X_{14} is an apolar amino acid;

X_{15} is an acidic amino acid;

X_{16} is a polar amino acid;

X_{17} is a basic amino acid; and

each " " between residues X_1 through X_{17} is independently an amide, a substituted amide or an isostere of amide.

16. (New) The method of Claim 14, wherein:

X_1 is Gly;

X_2 is Trp or Ala;

X_3 is Asp or Ala;

X_4 is His;

X_5 is Met;

X_6 is Phe;

X_7 is Thr;

X_8 is Val;

X_9 is Asp or Ala;

X_{10} is Phe;

X_{11} is Trp;

X_{12} is Thr;

X_{13} is Ile;

X_{14} is Met;

X_{15} is Glu;

X_{16} is Asn;

X_{17} is His or Ala;

Z_1 is H_2N-;

Z_2 is -C(O)OH; and

each "—" between residues X_1 through X_{17} is an amide linkage.

17. (New) A method of treating an iron overload disease, comprising administering to a subject a therapeutically effective amount of a compound comprising the formula:

(I) Z_1-X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-X_{15}-X_{16}-X_{17}-Z_2

wherein:

X_1 is an apolar residue;

X_2 is a hydrophobic residue;

X_3 is an acidic or an aliphatic residue;

X_4 is a basic residue;

X_5 is an apolar residue;

X_6 is an aromatic residue;

X_7 is a polar residue;

X_8 is an aliphatic residue;

X_9 is an acidic or an aliphatic residue;

X_{10} is an aromatic residue;

X_{11} is an aromatic residue;

X_{12} is a polar residue;

X_{13} is Ile;

X_{14} is an apolar residue;

X_{15} is an acidic residue;

X_{16} is a polar residue;

X_{17} is a basic or an aliphatic residue;

Z_1 is H_2N-, RHN- or, RRN-;

Z_2 is -C(O)R, -C(O)OR, -C(O)NHR, -C(O)NRR;

each R is independently (C_1-C_6) alkyl, (C_1-C_6) alkenyl, (C_1-C_6) alkynyl, substituted (C_1-C_6) alkyl, substituted (C_1-C_6) alkenyl or substituted (C_1-C_6) alkynyl;

each "—" between residues Z_1 and X_1 and residues Z_2 and X_{17} represents a covalent linkage; and

each "—" between residues X_1 through X_{17} represents a covalent linkage,

wherein the compound reduces cell-associated binding of transferrin as measured in an *in vitro* cellular binding assay and produces at least an additive effect with soluble HFE/β_2m heterodimers in reducing cell-associated binding of transferrin as measured in the assay.

18. (New) The method of Claim 17, wherein:

X_1 is an apolar amino acid;

X_2 is an aromatic amino acid;

X_3 is an acidic amino acid;

X_4 is a basic amino acid;

X_5 is an apolar amino acid;

X_6 is an aromatic amino acid;

X_7 is a polar amino acid;

X_8 is a aliphatic amino acid;

X_9 is a an acidic amino acid;

X_{10} is an aromatic amino acid;

X_{11} is an aromatic amino acid;

X_{12} is a polar amino acid;

X_{13} is Ile;

X_{14} is an apolar amino acid;

X_{15} is an acidic amino acid;

X_{16} is a polar amino acid;

X_{17} is a basic amino acid; and

each "—" between residues X_1 through X_{17} is independently an amide, a substituted amide or an isostere of amide.

19. (New) The method of Claim 17, wherein:

X_1 is Gly;

X_2 is Trp or Ala;

X_3 is Asp or Ala;

X_4 is His;

X_5 is Met;

X_6 is Phe;

X_7 is Thr;

X_8 is Val;